



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/786,445A

DATE: 07/26/2004

TIME: 15:28:04

Input Set : A:\096429-9141.txt

Output Set: N:\CRF4\07262004\J786445A.raw

3 <110> APPLICANT: Welch, Rodney A.  
 4 Lathem, Wyndham W.  
 5 Grys, Thomas E.  
 7 <120> TITLE OF INVENTION: E. COLI O157:H7 C1-INH-BINDING PROTEIN AND METHODS OF USE  
 9 <130> FILE REFERENCE: 096429-9141  
**C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/786,445A**  
 12 <141> CURRENT FILING DATE: 2004-02-25  
 14 <150> PRIOR APPLICATION NUMBER: 10/002,309  
 15 <151> PRIOR FILING DATE: 2001-10-26  
 17 <150> PRIOR APPLICATION NUMBER: 60/243,675  
 18 <151> PRIOR FILING DATE: 2000-10-26  
 20 <160> NUMBER OF SEQ ID NOS: 25  
 22 <170> SOFTWARE: PatentIn version 3.1  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 2798  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Unknown  
 29 <220> FEATURE:  
 30 <223> OTHER INFORMATION: Description of Unknown Organism: E. coli O157:H7 plasmid  
 pO157  
 32 <220> FEATURE:  
 33 <221> NAME/KEY: CDS  
 34 <222> LOCATION: (138)..(2798)  
 35 <223> OTHER INFORMATION:  
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 41 ctgaaaaaat aaaatataga aatactgtta tatccggctg catgaacact aaaatgaatg 120  
 43 agagatggag aacacccg atg aaa tta aag tat ctg tca tgt acg atc ctt 170  
 44 Met Lys Leu Lys Tyr Leu Ser Cys Thr Ile Leu  
 45 1 5 10  
 47 gcc cct ctg gcg att ggg gta ttt tct gca aca gct gct gat aat aat 218  
 48 Ala Pro Leu Ala Ile Gly Val Phe Ser Ala Thr Ala Ala Asp Asn Asn  
 49 15 20 25  
 51 tca gcc att tat ttc aat acc tcc cag cct ata aat gat ctg cag ggt 266  
 52 Ser Ala Ile Tyr Phe Asn Thr Ser Gln Pro Ile Asn Asp Leu Gln Gly  
 53 30 35 40  
 55 tcg ttg gcc gca gag gtg aaa ttt gca caa agc cag att tta ccc gcc 314  
 56 Ser Leu Ala Ala Glu Val Lys Phe Ala Gln Ser Gln Ile Leu Pro Ala  
 57 45 50 55  
 59 cat cct aaa gaa ggg gat agt caa cca cat ctg acc agc ctg cggtaaa 362  
 60 His Pro Lys Glu Gly Asp Ser Gln Pro His Leu Thr Ser Leu Arg Lys  
 61 60 65 70 75  
 63 agt ctg ctg ctt gtc cgt ccg gtg aaa gct gat gat aaa aca cct gtt 410  
 64 Ser Leu Leu Val Arg Pro Val Lys Ala Asp Asp Lys Thr Pro Val



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65	80	85	90	
67 cag gtg gaa gcc cgc gat gat aat aat aaa att ctc ggt acg tta acc				458
68 Gln Val Glu Ala Arg Asp Asp Asn Asn Lys Ile Leu Gly Thr Leu Thr				
69 95 100 105				
71 ctt tat cct cct tca tca cta ccg gat aca atc tac cat ctg gat ggt				506
72 Leu Tyr Pro Pro Ser Ser Leu Pro Asp Thr Ile Tyr His Leu Asp Gly				
73 110 115 120				
75 gtt ccg gaa ggt ggt atc gat ttc aca cct cat aat gga acg aaa aag				554
76 Val Pro Glu Gly Gly Ile Asp Phe Thr Pro His Asn Gly Thr Lys Lys				
77 125 130 135				
79 atc att aat acg gtg gct gaa gta aac aaa ctc agt gat gcc agc ggg				602
80 Ile Ile Asn Thr Val Ala Glu Val Asn Lys Leu Ser Asp Ala Ser Gly				
81 140 145 150 155				
83 agt tct att cat agc cat cta aca aat aat gca ctg gtg gag atc cat				650
84 Ser Ser Ile His Ser His Leu Thr Asn Asn Ala Leu Val Glu Ile His				
85 160 165 170				
87 act gca aat ggt cgt tgg gta aga gac att tat ctg ccg cag gga ccc				698
88 Thr Ala Asn Gly Arg Trp Val Arg Asp Ile Tyr Leu Pro Gln Gly Pro				
89 175 180 185				
91 gac ctt gaa ggt aag atg gtt cgc ttt gtt tcg tct gca ggc tat agt				746
92 Asp Leu Glu Gly Lys Met Val Arg Phe Val Ser Ser Ala Gly Tyr Ser				
93 190 195 200				
95 tca acg gtt ttt tat ggt gat cga aaa gtc aca ctc tcg gtg ggt aac				794
96 Ser Thr Val Phe Tyr Gly Asp Arg Lys Val Thr Leu Ser Val Gly Asn				
97 205 210 215				
99 act ctt ctg ttc aaa tat gta aat ggt cag tgg ttc cgc tcc ggt gaa				842
100 Thr Leu Leu Phe Lys Tyr Val Asn Gly Gln Trp Phe Arg Ser Gly Glu				
101 220 225 230 235				
103 ctg gag aat aat cga atc act tat gct cag cat att tgg agt gct gaa				890
104 Leu Glu Asn Asn Arg Ile Thr Tyr Ala Gln His Ile Trp Ser Ala Glu				
105 240 245 250				
107 ctg cct gcg cac tgg atc gtg cct ggt tta aac ttg gtg att aaa cag				938
108 Leu Pro Ala His Trp Ile Val Pro Gly Leu Asn Leu Val Ile Lys Gln				
109 255 260 265				
111 ggc aat ctg agc ggt cgc cta aat gat atc aag att gga gca ccg ggt				986
112 Gly Asn Leu Ser Gly Arg Leu Asn Asp Ile Lys Ile Gly Ala Pro Gly				
113 270 275 280				
115 gag ctg ttg cat aca att gat atc ggg atg ttg acc act ccc cgg				1034
116 Glu Leu Leu Leu His Thr Ile Asp Ile Gly Met Leu Thr Thr Pro Arg				
117 285 290 295				
119 gat cgc ttt gat ttt gcc aaa gac aaa gaa gca cat agg gaa tat ttc				1082
120 Asp Arg Phe Asp Phe Ala Lys Asp Lys Glu Ala His Arg Glu Tyr Phe				
121 300 305 310 315				
123 cag acc att cct gta agt cgt atg att gtt aat aat tat gcg cct cta				1130
124 Gln Thr Ile Pro Val Ser Arg Met Ile Val Asn Asn Tyr Ala Pro Leu				
125 320 325 330				
127 cac cta aag gaa gtt atg tta cca acc gga gag tta ttg aca gat atg				1178
128 His Leu Lys Glu Val Met Leu Pro Thr Gly Glu Leu Leu Thr Asp Met				
129 335 340 345				

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131 gat cca gga aat ggt ggg tgg cat agt ggt aca atg cgt caa aga ata	1226
132 Asp Pro Gly Asn Gly Gly Trp His Ser Gly Thr Met Arg Gln Arg Ile	
133       350                   355                   360	
135 ggt aaa gaa ttg gtt tcg cat ggc att gat aat gct aac tat ggt tta	1274
136 Gly Lys Glu Leu Val Ser His Gly Ile Asp Asn Ala Asn Tyr Gly Leu	
137       365                   370                   375	
139 aat agt acc gca ggc tta ggg gag aat agt cat cca tat gta gtt gcg	1322
140 Asn Ser Thr Ala Gly Leu Gly Glu Asn Ser His Pro Tyr Val Val Ala	
141       380                   385                   390                   395	
143 caa tta gcg gca cat aat agc cgc ggt aat tat gct aat ggc atc cag	1370
144 Gln Leu Ala Ala His Asn Ser Arg Gly Asn Tyr Ala Asn Gly Ile Gln	
145       400                   405                   410	
147 gtt cat ggt ggc tcc gga ggt ggg gga att gtt act tta gat tcc aca	1418
148 Val His Gly Gly Ser Gly Gly Ile Val Thr Leu Asp Ser Thr	
149       415                   420                   425	
151 ttg ggg aat gag ttc agt cat gaa gtt ggt cat aat tat ggt ctt ggt	1466
152 Leu Gly Asn Glu Phe Ser His Glu Val Gly His Asn Tyr Gly Leu Gly	
153       430                   435                   440	
155 cat tat gta gat ggt ttc aag ggt tct gta cat cgt agt gca gaa aat	1514
156 His Tyr Val Asp Gly Phe Lys Gly Ser Val His Arg Ser Ala Glu Asn	
157       445                   450                   455	
159 aac aac tca act tgg gga tgg gat ggt gat aaa aac cgg ttt att cct	1562
160 Asn Asn Ser Thr Trp Gly Trp Asp Gly Asp Lys Lys Arg Phe Ile Pro	
161       460                   465                   470                   475	
163 aac ttt tat ccg tct caa aca aat gaa aag agt tgt ctg aat aat cag	1610
164 Asn Phe Tyr Pro Ser Gln Thr Asn Glu Lys Ser Cys Leu Asn Asn Gln	
165       480                   485                   490	
167 tgt caa gaa ccg ttt gat gga cac aaa ttt ggt ttt gac gcc atg gcg	1658
168 Cys Gln Glu Pro Phe Asp Gly His Lys Phe Gly Phe Asp Ala Met Ala	
169       495                   500                   505	
171 gga ggc agc cct ttc tct gct gca aac cgt ttc aca atg tat act ccg	1706
172 Gly Gly Ser Pro Phe Ser Ala Ala Asn Arg Phe Thr Met Tyr Thr Pro	
173       510                   515                   520	
175 aat tca tcg gct atc atc cag cgt ttt ttt gaa aat aac gct gtg ttc	1754
176 Asn Ser Ser Ala Ile Ile Gln Arg Phe Phe Glu Asn Lys Ala Val Phe	
177       525                   530                   535	
179 gat agc cgt tcc tcc acc ggc ttc agc aag tgg aat gca gat acg cag	1802
180 Asp Ser Arg Ser Ser Thr Gly Phe Ser Lys Trp Asn Ala Asp Thr Gln	
181       540                   545                   550                   555	
183 gaa atg gaa ccg tat gaa cac acc att gac cgt gcg gag cag att acg	1850
184 Glu Met Glu Pro Tyr Glu His Thr Ile Asp Arg Ala Glu Gln Ile Thr	
185       560                   565                   570	
187 gct tca gtc aat gag cta agt gaa agc aac atg gct gag ctg atg gca	1898
188 Ala Ser Val Asn Glu Leu Ser Glu Ser Lys Met Ala Glu Leu Met Ala	
189       575                   580                   585	
191 gag tac gct gtc gtc aaa gtg cat atg tgg aac ggt aac tgg aca aga	1946
192 Glu Tyr Ala Val Val Lys Val His Met Trp Asn Gly Asn Trp Thr Arg	
193       590                   595                   600	
195 aac atc tat atc cct aca gcc tcc gca gat aat aga ggc agt atc ctg	1994

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196 Asn Ile Tyr Ile Pro Thr Ala Ser Ala Asn Arg Gly Ser Ile Leu		
197 605 610 615		
199 acc atc aac cat gag gcc ggt tat aat agt tat ctg ttt ata aat ggt		2042
200 Thr Ile Asn His Glu Ala Gly Tyr Asn Ser Tyr Leu Phe Ile Asn Gly		
201 620 625 630 635		
203 gac gaa aag gtc gtt tcc cag ggg tat aaa aag agc ttt gtt tcc gat		2090
204 Asp Glu Lys Val Val Ser Gln Gly Tyr Lys Lys Ser Phe Val Ser Asp		
205 640 645 650		
207 ggt cag ttc tgg aaa gaa cgt gat gtg gtt gat act cgt gaa gcg cgt		2138
208 Gly Gln Phe Trp Lys Glu Arg Asp Val Val Asp Thr Arg Glu Ala Arg		
209 655 660 665		
211 aag cca gag cag ttt ggt gtt cct gtg acg acc ctg gtg ggg tat tac		2186
212 Lys Pro Glu Gln Phe Gly Val Pro Val Thr Thr Leu Val Gly Tyr Tyr		
213 670 675 680		
215 gat ccg gaa ggc acg ctg tca agc tac atc tat cct gcg atg tat ggt		2234
216 Asp Pro Glu Gly Thr Leu Ser Ser Tyr Ile Tyr Pro Ala Met Tyr Gly		
217 685 690 695		
219 gcc tat ggc ttc act tat tcc gat gat agt cag aat cta tcc gat aac		2282
220 Ala Tyr Gly Phe Thr Tyr Ser Asp Asp Ser Gln Asn Leu Ser Asp Asn		
221 700 705 710 715		
223 gac tgc cag ctg cag gtg gat acg aaa gaa ggg cag ttg cga ttc aga		2330
224 Asp Cys Gln Leu Gln Val Asp Thr Lys Glu Gly Gln Leu Arg Phe Arg		
225 720 725 730		
227 ctg gct aat cac cgg gct aac aac act gta atg aat aag ttc cat att		2378
228 Leu Ala Asn His Arg Ala Asn Asn Thr Val Met Asn Lys Phe His Ile		
229 735 740 745		
231 aac gtg cca aca gaa agt cag ccc aca cag gcc aca ttg gtt tgc aat		2426
232 Asn Val Pro Thr Glu Ser Gln Pro Thr Gln Ala Thr Leu Val Cys Asn		
233 750 755 760		
235 aac aag ata ctg gat acc aaa tcg ctc aca cct gcg cca gaa gga ctt		2474
236 Asn Lys Ile Leu Asp Thr Lys Ser Leu Thr Pro Ala Pro Glu Gly Leu		
237 765 770 775		
239 acc tat act gta aat ggg cag gca ctt cca gca aaa gaa aac gag gga		2522
240 Thr Tyr Thr Val Asn Gly Gln Ala Leu Pro Ala Lys Glu Asn Glu Gly		
241 780 785 790 795		
243 tgc atc gtg tcc gtg aat tca ggt aaa cgt tac tgt ttg ccg gtt ggt		2570
244 Cys Ile Val Ser Val Asn Ser Gly Lys Arg Tyr Cys Leu Pro Val Gly		
245 800 805 810		
247 caa cgg tca gga tat agc ctt cct gac tgg att gtt ggg cag gaa gtc		2618
248 Gln Arg Ser Gly Tyr Ser Leu Pro Asp Trp Ile Val Gly Gln Glu Val		
249 815 820 825		
251 tat gtc gac agc ggg gct aaa gcg aaa gtg ctg ctt tct gac tgg gat		2666
252 Tyr Val Asp Ser Gly Ala Lys Ala Lys Val Leu Leu Ser Asp Trp Asp		
253 830 835 840		
255 aac ctg tcc tat aac agg att ggt gag ttt gta ggt aat gtg aac cca		2714
256 Asn Leu Ser Tyr Asn Arg Ile Gly Glu Phe Val Gly Asn Val Asn Pro		
257 845 850 855		
259 gct gat atg aaa aaa gtt aaa gcc tgg aac gga cag tat ttg gac ttc		2762
260 Ala Asp Met Lys Lys Val Lys Ala Trp Asn Gly Gln Tyr Leu Asp Phe		

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261 860                    865                    870                    875  
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 265                    880                    885  
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 269 <211> LENGTH: 886  
 270 <212> TYPE: PRT  
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 273 <220> FEATURE:  
 274 <223> OTHER INFORMATION: Description of Unknown Organism: E. coli O157:H7 plasmid  
 pO157  
 276 <400> SEQUENCE: 2  
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 283                    20                    25                    30  
 286 Asn Thr Ser Gln Pro Ile Asn Asp Leu Gln Gly Ser Leu Ala Ala Glu  
 287                    35                    40                    45  
 290 Val Lys Phe Ala Gln Ser Gln Ile Leu Pro Ala His Pro Lys Glu Gly  
 291                    50                    55                    60  
 294 Asp Ser Gln Pro His Leu Thr Ser Leu Arg Lys Ser Leu Leu Leu Val  
 295 65                    70                    75                    80  
 298 Arg Pro Val Lys Ala Asp Asp Lys Thr Pro Val Gln Val Glu Ala Arg  
 299                    85                    90                    95  
 302 Asp Asp Asn Asn Lys Ile Leu Gly Thr Leu Thr Leu Tyr Pro Pro Ser  
 303                    100                    105                    110  
 306 Ser Leu Pro Asp Thr Ile Tyr His Leu Asp Gly Val Pro Glu Gly Gly  
 307                    115                    120                    125  
 310 Ile Asp Phe Thr Pro His Asn Gly Thr Lys Lys Ile Ile Asn Thr Val  
 311                    130                    135                    140  
 314 Ala Glu Val Asn Lys Leu Ser Asp Ala Ser Gly Ser Ser Ile His Ser  
 315 145                    150                    155                    160  
 318 His Leu Thr Asn Asn Ala Leu Val Glu Ile His Thr Ala Asn Gly Arg  
 319                    165                    170                    175  
 322 Trp Val Arg Asp Ile Tyr Leu Pro Gln Gly Pro Asp Leu Glu Gly Lys  
 323                    180                    185                    190  
 326 Met Val Arg Phe Val Ser Ser Ala Gly Tyr Ser Ser Thr Val Phe Tyr  
 327                    195                    200                    205  
 330 Gly Asp Arg Lys Val Thr Leu Ser Val Gly Asn Thr Leu Leu Phe Lys  
 331                    210                    215                    220  
 334 Tyr Val Asn Gly Gln Trp Phe Arg Ser Gly Glu Leu Glu Asn Asn Arg  
 335 225                    230                    235                    240  
 338 Ile Thr Tyr Ala Gln His Ile Trp Ser Ala Glu Leu Pro Ala His Trp  
 339                    245                    250                    255  
 342 Ile Val Pro Gly Leu Asn Leu Val Ile Lys Gln Gly Asn Leu Ser Gly  
 343                    260                    265                    270  
 346 Arg Leu Asn Asp Ile Lys Ile Gly Ala Pro Gly Glu Leu Leu Leu His  
 347                    275                    280                    285  
 350 Thr Ile Asp Ile Gly Met Leu Thr Thr Pro Arg Asp Arg Phe Asp Phe  
 351                    290                    295                    300

**VERIFICATION SUMMARY**

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L:11 M:270 C: Current Application Number differs, Wrong Format

L:38 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:35

L:700 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:18,Line#:697